

FIG. 1

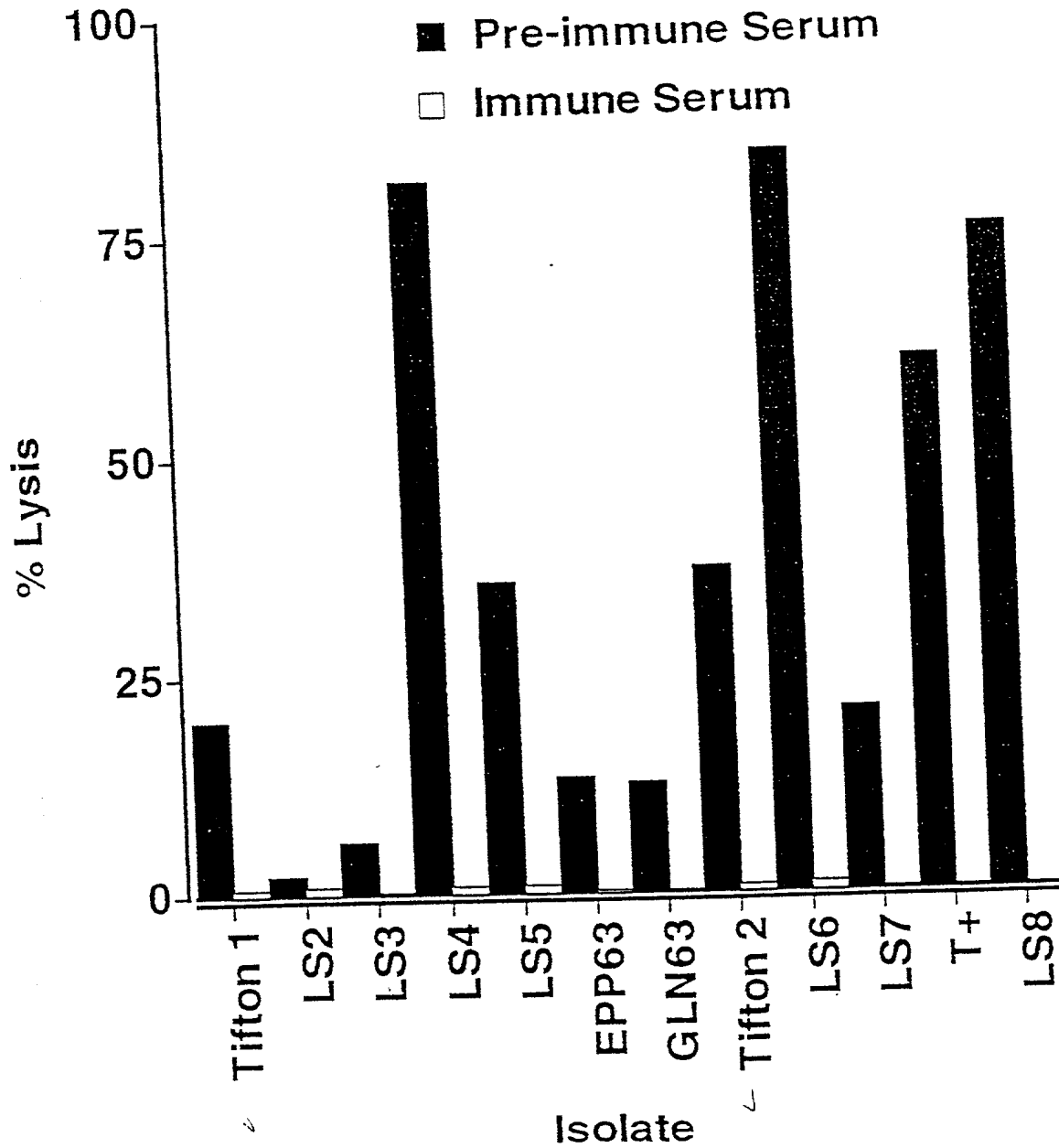
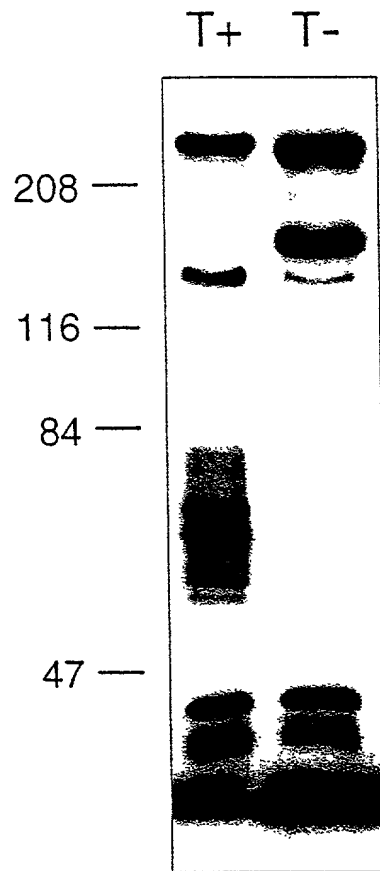


FIG. 2



Appendix A update-July 1999

$$\begin{array}{r} m \times A \\ + \\ M \times A \\ \hline \end{array}$$

Appendix A update-July 1999, continued

Bases 1201-2400

Amino acids 401-800

1201	AAAATTTTAGAGTGGGAAAAGCAAATGGCGGTCAGAACTATTTTGATAAAGGCTATGAT	1260
401	K I L E W E K Q N G G Q N Y F D K G Y D	420
1261	TCTCGTTATGCTGCTTATTTAGCTAATAACTTAAATTTTTGTCTGAGCTAAATAAGAG	1320
421	S R Y A A Y L A N N L K F L S E L N K E	440
1321	TTGGAAGCTGAACGTGTTATTGCAATCACCCAACAACGTTGGGATAATAATATTGGTGAG	1380
441	L E A E R V I A I T Q Q R W D N N I G E	460
1381	TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGGAAAAGCTTATGCAGATGCT	1440
461	L A G I T K L G E R I K S G K A Y A D A	480
1441	TTTGAAGATGGCAAGAAAGTTGAAGCTGGTTCCAATATTACTTTGGATGCTAAACTGGT	1500
481	F E D G K K V E A G S N I T L D A K T G	500
1501	ATCATAGACATTAGTAATTCAAATGGGAAAAAACGCAAGCGTTGCATTTCACTTCGCCT	1560
501	I I D I S N S N G K K T Q A L H F T S P	520
1561	TTGTTAACAGCAGGAAGTGAATCACGTGAACGTTTAACTAATGGTAAATACTCTTATATT	1620
521	L L T A G T E S R E R L T N G K Y S Y I	540
1621	AATAAGTTAAAATTCGGACGTGTAATAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT	1680
541	N K L K F G R V K N W Q V T D G E A S S	560
1681	AAATTAGATTTCTCTAAAGTTATTCAGCGTGTAGCCGAGACAGAAGGCACAGACGAGATT	1740
561	K L D F S K V I Q R V A E T E G T D E I	580
1741	GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTTGTTGGTCAAGGTAAAATG	1800
581	G L I V N A K A G N D D I F V G Q G K M	600
1801	AATATTGATGGTGGAGATGGACACGATCGTGTCTTCTATAGTAAAGACGGAGGATTTGGT	1860
601	N I D G G D G H D R V F Y S K D G G F G	620
1861	AATATTACTGTAGATGGTACGAGTGAACAGAAGCAGGCAGTTATACAGTTAATCGTAAG	1920
621	N I T V D G T S A T E A G S Y T V N R K	640
1921	GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGGTAAA	1980
641	V A R G D I Y H E V V K R Q E T K V G K	660
1981	CGTACTGAAACTATCCAGTATCGTGATTATGAATTAAGAAAAGTTGGGTATGGTTATCAG	2040
661	R T E T I Q Y R D Y E L R K V G Y G Y Q	680
2041	TCTACCGATAATTTGAAATCAGTAGAAGAAGTAATTGGTTCTCAATTTAATGATGTATTC	2100
681	S T D N L K S V E E V I G S Q F N D V F	700
2101	AAAGGTTCTAAATTCAACGACATATTCATAGTGGTGAAGGTGATGATTTACTCGATGGT	2160
701	K G S K F N D I F H S G E G D D L L D G	720
2161	GGTGCTGGTGACGACCGCTTGTGTTGGTAAAGGCAACGATCGACTTTCTGGAGATGAA	2220
721	G A G D D R L F G G K G N D R L S G D E	740
2221	GGCGATGATTTACTCGATGGCGGTTCTGGTGATGATGATTAATGGTGGTGCTGGTAAT	2280
741	G D D L L D G G S G D D V L N G G A G N	760
2281	GATGTCTATATCTTTGCGAAAGGTGATGGTAATGATACTTTGTACGATGGCACGGGCAAT	2340
761	D V Y I F R K G D G N D T L Y D G T G N	780
2341	GATAAATTAGCATTTGCAGATGCAAAATATCTGATATTATGATTGAACGTACCAAAGAG	2400
781	D K L A F A D A N I S D I M I E R T K E	800

1201-2400 bases

Appendix A update-July 1999, continued

Bases 2401-2784

Amino acids 801-927

2401	GGTATTATAGTTAAACGAAATGATCATTGAGGTAGTATTAACATACCAAGATGGTACATA	2460
801	G I I V K R N D H S G S I N I P R W Y I	820
2461	ACATCAAATTTACAAAATTATCAAAGTAATAAAACAGATCATAAAATTGAGCAACTAATT	2520
821	T S N L Q N Y Q S N K T D H K I E Q L I	840
2521	GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTTTGCAAGATAAGAAA	2580
841	G K D G S Y I T S D Q I D K I L Q D K K	860
2581	GATGGTACAGTAATTACATCTCAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCCAA	2640
861	D G T V I T S Q E L K K L A D E N K S Q	880
2641	AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA	2700
881	K L S A S D I A S S L N K L V G S M A L	900
2701	TTTGGTACAGCAAATAGTGTGAGTTCTAACGCCTTACAGCCAATTACACAACCAACTCAA	2760
901	F G T A N S V S S N A L Q P I T Q P T Q	920
2761	GGAATTTTGGCTCCAAGTGTTTAG	2784
921	G I L A P S V *	928

SEQ ID NO: 1
SEQ ID NO: 2

[illegible]

MbxA	P	S	V	-	-	-	-	-	-	-	-	927
LktA	Q	S	L	S	S	S	Q	E	A	R	A	953
ApxIIA	V	S	.	N	N	I	Q	L	A	R	A	956
HlyA	Y	G	R	N	S	I	T	L	T	A	S	1023

FIG. 5

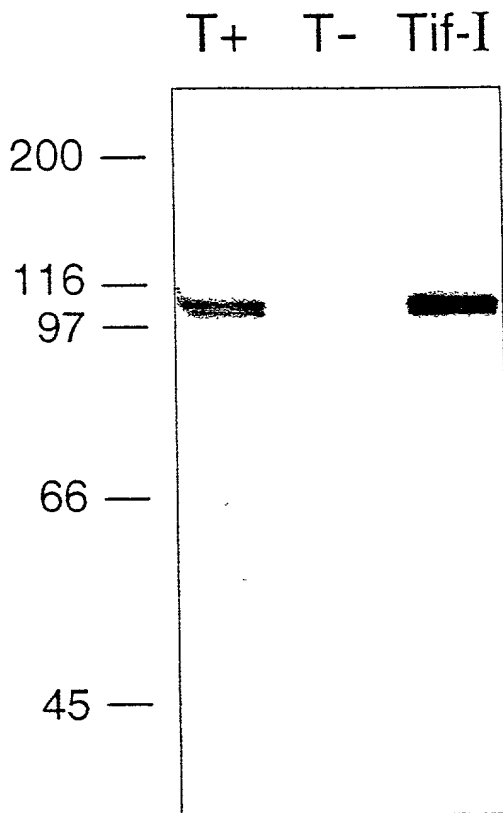


FIG. 6

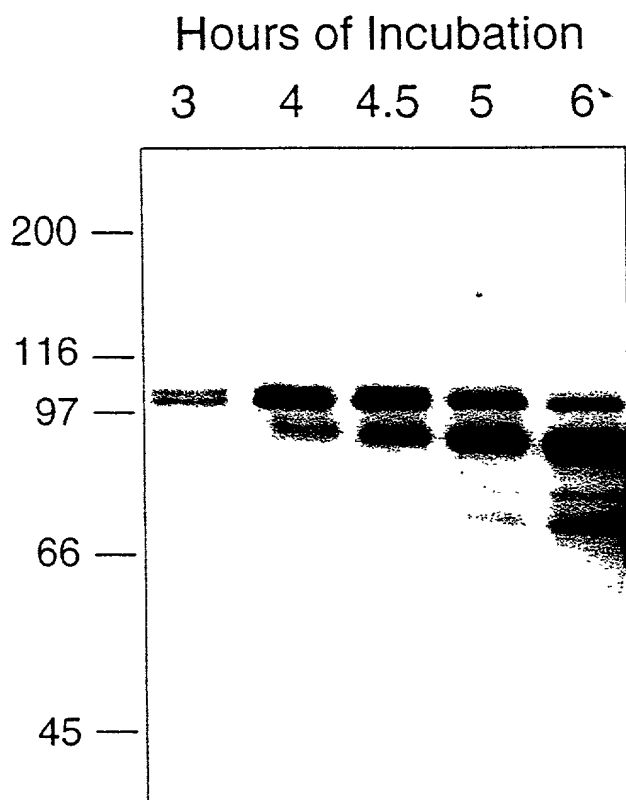
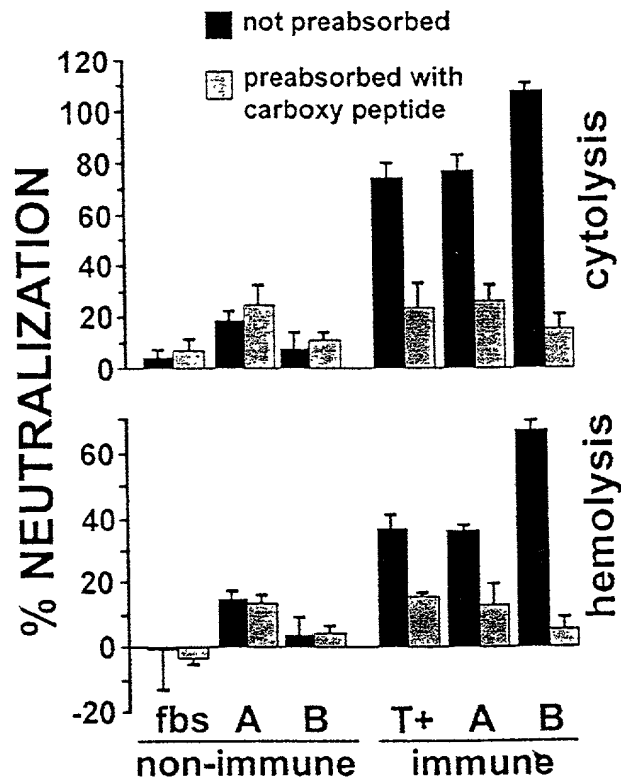


FIG. 7



1 ATGGGTGGTGATACTTCTTTAATTAGACTTAATTTACAAACCCTTAATAGTAATTTAGTT 60
 1 M G G D T S L I R L N L Q T L N S N L V 20
 61 ATGATAGATTATGCTCAACAACCTGCTCTATCTGCTCTGTTATCCTTGCCAAATACTAT 120
 21 M I D Y A Q Q P A L S A L V I L A K Y Y 40
 121 GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTTCTGATAATACAAAAGGAGAC 180
 41 G I S A S P A D I M H Q F S D N T K G D 60
 181 CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAAGGTAAAGATTATA 240
 61 L N E I E W M L A A K K L E L K V K I I 80
 241 AAACAGCCTTTAACTCGATTGTCAATGATAACACTTCCTGCTTTGGTGTGGTGTGATAAT 300
 81 K Q P L T R L S M I T L P A L V W C D N 100
 301 AAGCCCGATTAGATCAAAATTTAACTCTCATTTTATACTAACTAAAATTGATGGGGTG 360
 101 K P D L D Q N L N S H F I L T K I D G V 120
 361 GGATCTGCTGCAAAATATCTCATCTACGATTTGATTGAGAATCGTCCATAATATTAGAT 420
 121 G S A A K Y L I Y D L I E N R P I I L D 140
 421 GCAAGTGAGTTTTCTGAAAGATATTCTGGTAAGTTAATGCTAGTAACTTCCCGTGGTCA 480
 141 A S E F S E R Y S G K L M L V T S R A S 160
 481 ATATTGGGTTCATTGGCTAAATTTGATTTTACTTGGTTTATTCCTGCGTAATCAAATAT 540
 161 I L G S L A K F D F T W F I P A V I K Y 180
 541 CGTTATATTTTTTTGAAGTCATCGTTATTTTCACTGGTGTACAGATTTTTGCTCTGATT 600
 181 R Y I F F E V I V I S V V L Q I F A L I 200
 601 ACGCCATTGTTTTTTCAGGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTTTCTACT 660
 201 T P L F F Q V V M D K V L V H R G F S T 220
 661 CTGGATGTGGTAGCGATTGCCTTGTGGTAGTAAGTTTATTTGAAGTCATTTTAAAGTGGT 720
 221 L D V V A I A L L V V S L F E V I L S G 240
 721 CTACGCACTTATATTTTTGCTCATACAACCTCTCGAATTGATGTAGAGCTAGGAGCACGA 780
 241 L R T Y I F A H T T S R I D V E L G A R 260
 781 TTATTTTCGTCATCTATTAGCTCTACCGCTTGCTTATTTTGAAGTAGAAGAGTAGGCGAT 840
 261 L F R H L L A L P L A Y F E S R R V G D 280
 841 ACAGTTGCACGTATACGTGAATTGGAACATATCCGCAATTTCTTAACTGGTCAAGCTCTC 900
 281 T V A R I R E L E H I R N F L T G Q A L 300
 901 ACTTCAGTTTTAGATTTGGTGTCTTTTATATTCTTGTGTGAATGTGGTATTACAGC 960
 301 T S V L D L V F S F I F L F V M W Y Y S 320
 961 CCTACTTTAACTGCTAGTTTTGGCATCATTACCAATATATGCGTTTTGGTCTGCCTTT 1020
 321 P T L T L V V L A S L P I Y A F W S A F 340
 1021 ATTAGCCCAATTTTACGCACTCGACTAAATGATCAATTTGCACGCAATGCAGATAATCAA 1080
 341 I S P I L R T R L N D Q F A R N A D N Q 360
 1081 TCTTTTTTAGTGGAAAGTATTACTGCGGTTGGTACGGTAAAAGCAATGGCAGTTGAACCT 1140
 361 S F L V E S I T A V G T V K A M A V E P 380
 1141 CAAATGACCCGCTCGCTGGGATAATCAATTAGCAGCTTATGTGGTTTCTAGTTTTCGGGTA 1200
 381 Q M T R R W D N Q L A A Y V V S S F R V 400
 1201 GCTAAGTTGGCAATGGTTGGGAGCAAGGAGTACAACCTCATTCAAAGATGGTTATTGTG 1260
 401 A K L A M V G Q Q G V Q L I Q K M V I V 420
 1261 GCAACTCTATGGATTGGTGCAAAATTGGTAATTGAAGGCAAGCTATCGGTAGGTCAATTA 1320
 421 A T L W I G A K L V I E G K L S V G Q L 440

mxb
 mxb

FIG 8-1

1321	ATAGCATTTAATATGCTGGCAGGTGAGTGGCCGCTCTGTTATCCGCCTGGCACAGCTA	1380
441	I A F N M L A G Q V A A P V I R' L A' Q L	460
1381	TGGCAAGATTTTCAGCAAGTAGGTATTTAGTGGCGAGATTGGGTGATATTTAAATACT	1440
461	W Q D F Q Q V G I S V A R L G D I L N T	480
1441	CCAAGTGGCATTCTACATCTCGCTTAACCTTACCTGATATTAAGGGTGATATTACATTT	1500
481	P T E H S T S R L T L P D I K G D I T F	500
1501	GAAATGTTGATTTTCGCTACAAAATAGATGGGCATTTAATATTACAGAATTTAAATTTA	1560
501	E N V D F R Y K I D G H L I L Q N L N L	520
1561	CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAGGTAAATCAACA	1620
521	Q I N A G E I L G I V G R S G S G K S T	540
1621	TTGACAAAATTAGTACAGCGTTTATATGTACCAGAAAATGGGCGAATATTAGTTGATGGA	1680
541	L T K L V Q R L Y V P E N G R I L V D G	560
1681	AACGATTTGGCATTAGCTGATCCCGCTTGGCTGCGTCGCCAAGTGGGTGTTGTTTTGCAG	1740
561	N D L A L A D P A W L R R Q V G V V L Q	580
1741	GAAATGTGTTACTCAATCGTAGTATTCGAGATAATATTGCCCTAACTGATACGGGCATG	1800
581	E N V L L N R S I R D N I A L T D T G M	600
1801	TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCTGGGGCACATGACTTTATTATGGAA	1860
601	S L E F I I Q A A K M S G A H D F I M E	620
1861	TTGCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTGAGGTGGACAA	1920
621	L P E G Y D T I V G E Q G A G L S G G Q	640
1921	CGCCAGCGTATCGCTATTGCGCGTGCTTTAATTACCAATCCGCGTATTTTGATTTTGTAT	1980
641	R Q R I A I A R A L I T N P R I L I F D	660
1981	GAAGCTACTAGTGCATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA	2040
661	E A T S A L D Y E S E R A I M Q N M Q A	680
2041	ATTTGCCAAGGTAGAACAGTGTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA	2100
681	I C Q G R T V L I I A H R L S T V K M A	700
2101	CATCGCATTATTGCAATGGACAAGGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG	2160
701	H R I I A M D K G K I V E Q G T H Q E L	720
2161	TTGCAAAAAGAAGATGGTTACTATCGTTATTTATATGATTTGCAGAATGGATAAA	2215
721	L Q K E D G Y Y R Y L Y D L Q N G *	739

F168-2

SEQ ID NO: 30
SEQ ID NO: 18

F15.9

Lkts	- - - - M	LD	AAQQP	APSA	TVILAKY	G	TSASPA	IM	HQFSNTR	RG	DNEIEN	L	AAKLEL	55		
ApX18	M - A N	Q R N D	L	GLVA	LSLSPEEL		EFDDDGAG		LSGAWLL		LDLTPAWLL		AAKLEL	56		
Hly8	MDPFR	ED	L	GLYA	ELLAQYEN		LAVERFEIR		KKFDLGRG		LDLTPAWLL		AAKLEL	55		
	MDSC	K	LD	L	GLYA		ELLAQYEN		SVRFEIR		LGFTSWLL		AAKLEL	55		
Mbx8	VVI	I I I	OP	TLSMHT	LP	ALVWCDNKP	DLDQNLNS		FILTRIDGV	GSAAKYLIV	DLI-NRP			116		
Lkts	KAKHI	KKAT		SRIHL	NLP	ALVWQDNGKE		FILTRIDV	T-NRRLI	NLPQDAP			107		
ApX18	KAKQV	KKAT		DRIL	PIAL	ALVWREDGKE		FILTRIDV	NRAKKELI	DLTHHP			106		
Hly8	KVAGV	KKAT		DRIL	PIAL	ALVWREDGKE		FILTRIVS	KKANR	DLTHHP			106		
Mbx8	ILL	AGEFS		ERTS	SCZML	VTORASILG	SLAKPFDFTW		FIPAVIRIR	YIFFEYIV				177		
Lkts	QILST	DESE		ACIR	GOIL	VISHASVVG	QLAKPFDFTW		FIPAVIRIR	KIP	SEILIV			168		
ApX18	RILEQAR	SE		SKHGG	IL	VASHASVVG	KLAKPFDFTW		FIPAVIRIR	KIP	SEILIV			167		
Hly8	NLEQSE	SE		ALYQGH	IL	ASHSSVAG	KLAKPFDFTW		FIPAVIRIR	KIP	SEILIV			167		
Mbx8	ALITPLFPQ			VUMDRVLV		RGYSTLV	AALLVVS		FEILSGLR	TYIPARST				238		
Lkts	ALITPLFPQ			VUMDRVLV		RGYSTLV	TVALAIV		FEIVLSGLR	TYIPARST				229		
ApX18	ALITPLFPQ			VUMDRVLV		RGYSTLV	TVALAIV		FEIVLSGLR	TYIPARST				228		
Hly8	ALITPLFPQ			VUMDRVLV		RGYSTLV	TVALAIV		FEIVLSGLR	TYIPARST				228		
Mbx8	ARLPRELLA			LPATFES	SR	RVGDTVAR	RELHILMF		LTGQALTSV	LDLVFSPF				299		
Lkts	AKLPRELLS			LPISYFENR		RVGDTVAR	RELDQIRMF		LTGQALTSV	LDLVFSPF				290		
ApX18	AKLPRELLA			LPISYFENR		RVGDTVAR	RELDQIRMF		LTGQALTSV	LDLVFSPF				289		
Hly8	AKLPRELLA			LPISYFES	SR	RVGDTVAR	RELDQIRMF		LTGQALTSV	LDLVFSPF				289		
Mbx8	SPRLTLVL	L		ASLP	HYAFW	SAPISPILE	TELNDQFAR		NADNQSPFLV	ESVTAIGT				360		
Lkts	SPRLTLVL	L		GSPL	PCYILW	SIPISPILE	RELDEKPAR		SADNQAPFLV	ESVTAINMI				351		
ApX18	SPRLTLVL	L		GSPL	PCYILW	SIPISPILE	RELDEKPAR		SADNQAPFLV	ESVTAINMI				350		
Hly8	SPRLTLVL	L		GSPL	PCYILW	SIPISPILE	RELDEKPAR		SADNQAPFLV	ESVTAINMI				350		
Mbx8	QMTTRWDNQ			LAAVYVSS	SF	RVAKLAMTG	QQGVQLIQR		MVIVATLW	GAKLVIEGK				421		
Lkts	QMTTRWDNQ			LAAVYVSS	SF	RVVTLATIG	QQGVQLIQR		TVMVINLWL	GAKLVIEGK				412		
ApX18	QMTTRWDNQ			LAAVYVSS	AGF	RVVTLATIG	QQGVQLIQR		TVMVINLWL	GAKLVIEGK				411		
Hly8	QMTTRWDNQ			LAAVYVSS	AGF	RVVTLATIG	QQGVQLIQR		TVMVINLWL	GAKLVIEGK				411		
Mbx8	AFNMLAGQV			AAPVIRLQ		LWQDPQQVG	ISVARLGDV		LNSPTESY	SLLTLP	IK			GDITFRN	482	
Lkts	AFNMLAGQV			AAPVIRLQ		LWQDPQQVG	ISVARLGDV		LNSPTESY	SLLTLP	IK			GDITFRN	473	
ApX18	AFNMLAGQV			AAPVIRLQ		LWQDPQQVG	ISVARLGDV		LNSPTESY	SLLTLP	IK			GDITFRN	472	
Hly8	AFNMLAGQV			AAPVIRLQ		LWQDPQQVG	ISVARLGDV		LNSPTESY	SLLTLP	IK			GDITFRN	472	
Mbx8	IRPRIKIDG			HLILQ	MLNL	QINAGE	IVGRSGSGR		STLTNLQR	LYFENGRT					543	
Lkts	IRPRIKIDG			HLILQ	MLNL	QINAGE	IVGRSGSGR		STLTNLQR	LYFENGRT					534	
ApX18	IRPRIKIDG			HLILQ	MLNL	QINAGE	IVGRSGSGR		STLTNLQR	LYFENGRT					533	
Hly8	IRPRIKIDG			HLILQ	MLNL	QINAGE	IVGRSGSGR		STLTNLQR	LYFENGRT					533	
Mbx8	ALADFAWLR			ROVGVVLQ		NVLLNRSIR	DIATL	TDG	MSSEFIQA	AKSGARDF					604	
Lkts	ALADFAWLR			ROVGVVLQ		NVLLNRSIR	DIATL	TDG	MSSEFIQA	AKSGARDF					595	
ApX18	ALADFAWLR			ROVGVVLQ		NVLLNRSIR	DIATL	TDG	MSSEFIQA	AKSGARDF					594	
Hly8	ALADFAWLR			ROVGVVLQ		NVLLNRSIR	DIATL	TDG	MSSEFIQA	AKSGARDF					594	
Mbx8	YDTIVGEQG			AGLSGGQR		RIATARAL	TSF	ILIFD	EATSALDYE	SERAIMQNM					QAICQGR	665
Lkts	YDTIVGEQG			AGLSGGQR		RIATARAL	TSF	ILIFD	EATSALDYE	SERAIMQNM					QAICQGR	656
ApX18	YDTIVGEQG			AGLSGGQR		RIATARAL	TSF	ILIFD	EATSALDYE	SERAIMQNM					QAICQGR	655
Hly8	YDTIVGEQG			AGLSGGQR		RIATARAL	TSF	ILIFD	EATSALDYE	SERAIMQNM					QAICQGR	655
Mbx8	TVIIIAHRL			STVKMAHRI		IAM	RGRIV	EQGKQELL	QKEDGYRY	LYDLONG	717					
Lkts	TVIIIAHRL			STVKMAHRI		IAM	RGRIV	EQGKQELL	QKEDGYRY	LYDLONG	708					
ApX18	TVIIIAHRL			STVKMAHRI		IAM	RGRIV	EQGKQELL	QKEDGYRY	LYDLONG	707					
Hly8	TVIIIAHRL			STVKMAHRI		IAM	RGRIV	EQGKQELL	QKEDGYRY	LYDLONG	707					

717
708
707
707

SERIDNO
SERIDNO
SERIDNO

SERIDNO: 18
SERIDNO: 19
SERIDNO: 20
SERIDNO: 21

FIG. 10

DNASIS Translation Editor [11-00 C gene.dna]

1	ATGACGAAAAAGTTTGCAGAGCTAGGTTTAATTGCATGGCTTTGGTCTAACTCTGATATG	60
1	M T K K F A E L G L I A W L W S N S D M	20
61	CATAAACATTGGACGTTGTCTTTGTTTGGACCAATGTTATCCGGCAATTGAGACAGGT	120
21	H K H W T L S L F A T N V I P A I E T G	40
121	CAATATGTTATATTGAAAAGAGAAGATATGCCTGTAGCATATTGTAGTTGGGCTAAACTT	180
41	Q Y V I L K R E D M P V A Y C S W A K L	60
181	AGTTTAGAAAACGAGGTAAATATATTAACGATGTTACTTCTCTTAAGTTAGATGACTGG	240
61	S L E N E V K Y I N D V T S L K L D D W	80
241	CAGTCAGGTGACCGAAACTGGTTTATTGACTGGATTGCTCCATTTGGCGATAGTCTTACA	300
81	Q S G D R N W F I D W I A P F G D S L T	100
301	CTCACAAAACACATGAGAACGTTATTTTCAGATGAATTGTTTAGAGCGATTCTGTAGAT	360
101	L T K H M R T L F S D E L F R A I R V D	120
361	GGAAATTCATCGCATGGTAAGATATCTGAATTTTATGGAAAGTCTGTTGATTCAAAATTA	420
121	G N S S H G K I S E F Y G K S V D S K L	140
421	GCCTCAAGAATATTTGCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT	480
141	A S R I F A Q Y H E D L T S K L S T Q N	160
481	AATTTTATTATATCTAAAGATAATTA	507
161	N F I I S K D N *	169

SEQ ID NO: 31
SEQ ID NO: 32

mbx C
Mbx C

[illegible]

SEQ ID NO: 2
SEQ ID NO: 3
SEQ ID NO: 5
SEQ ID NO: 7

FIG 12-1

1321 CCAGGAATGAATGTTACTGCTGAAATTAACAGGTAAACGTCGTGTTTGGATTATATA 1380
441 P G M N V T A E I K T G K R R V L D Y I 460

1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA 1428
461 L S P L Q T K V D E S F R E R * 476

SEA ID NO: 36 }
SEA ID NO 37 }

FIG. 12-2

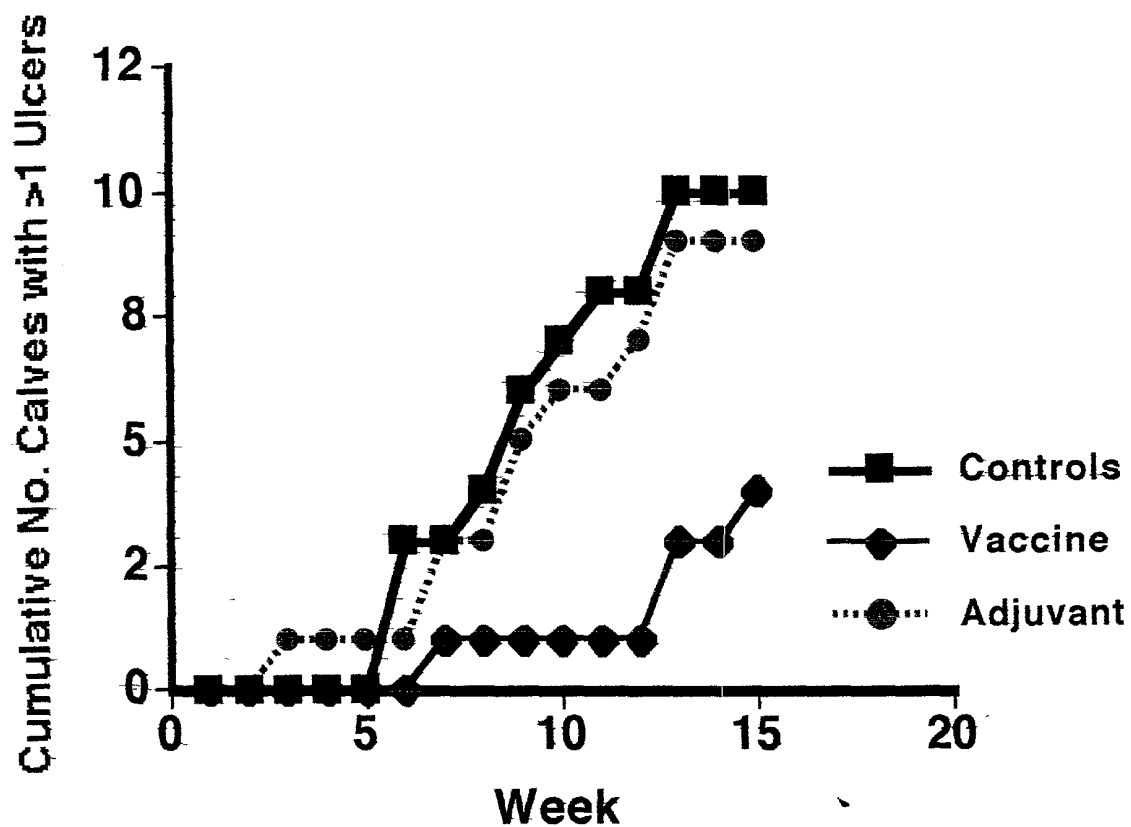
1321 CCAGGAATGAATGTTACTGCTGAAATTAACAGGTAAACGTCGTGTTTGGATTATATA 1380
441 P G M N V T A E I K T G K R R V L D Y I 460
1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA 1428
461 L S P L Q T K V D E S F R E R * 476

FIG. 13

MbxD	--MF--QA LK	FF RYITVWR	NTWA RDOLT	PPKRTK ELA	FLPAHLELT	48
LktD	MKIWLSG YE	PF LRYRN WA	EVWKIRK LD	HPNKRDESE	FLPAHLELIE	50
ApXID	MKTWLMGLYE	PFORIKTVWT	ELWKIRHOLD	TPDREKDENE	FLPAHLELIE	50
HlyD	MKTWLMGFS E	EL LRYKLVWS	ETWIRIRKOLD	TPVREKDENE	FLPAHLELIE	50
MbxD	TPVS RSS WT	AR IM FVL F	ALLWSNVGQ	IVATASGR	SSGSRSKTIQ	98
LktD	TPVS KKPRLI	AYLIMLPLVV	AVLASVSKV	EIVATAPGKL	TFSGRSKBIK	100
ApXID	TPVS KKPRLI	AYLIMLPLFL	ALV SIVSHV	EIVATATGKL	AFSDRSKEIK	100
HlyD	TPVS RKPRLI	AYFIMGFLVI	AF LSVLGQV	EIVATANGKL	TLSGRSKEIK	100
MbxD	S ETARVKA	V DGNV Q	G LVDLVG	GS DSDVAQSE	KALRAAQLSK	148
LktD	PIENAI VQEI	PVKDGGPVER	GQLLVSLTAL	GS DADI KKT M	ASLSLAKLEN	150
ApXID	PIENA VKEI	PVQDGGPVER	DQLLHLTAL	GADADQ QKT K	SSLSLTKLER	150
HlyD	PIENSIVKEI	IVK G SVRK	GDVLLKLTAL	GA ADTLKTQ	SSL LQA LLEQ	150
MbxD	LRL EA LSA	NHRINE QIDV	AYAKSL MIS	ESEINEAQT L	AQNQYQAWLA	197
LktD	YRYQTLLTAT	EKESLSEVIDL	.SRTEFNDSS	EEDRLRIKHL	IERQYTTWQN	199
ApXID	YRIE LLEA	AADRLPLI L	.TKDEFNHAT	EEDKTRI RYL	ITEQFEAWQN	199
HlyD	IRYQTLRSR I	ELNKLZPE KL	PDEPYFQNV S	EEV LR TSL	IKEQFSTWQN	200
MbxD	QDEQLKLT LK	GHAE LQ SAR	SQEQLNV SVG	AI EH KTD D	RSLKAENFIS	247
LktD	QKTOKELAYR	RREABKQTI F	AY RKYE G S	RIEQEK LKDF	KALYKQKS S	249
ApXID	QKYQKELALQ	R EAKQT L	ANIRKYE G S	RVENERL KDL	KKLFNSKSTS	249
HlyD	QKYQKELNLD	KRAE L TIL	ARIN YENVS	RVEKSRLDDF	RSL LHKQATA	250
MbxD	EHAYLEQESK	L SNQNLQS	TRSQ OKINA	AI QAE NRM	LYTONLKRDT	297
LktD	RHEL LAQENK	LIEAQN AVAV	YRSKLNE EN	DL LN VKEELE	LITOFFKSDT	299
ApXID	KHDVLTQESK	HIEAVNEI AV	YKSRLNE ES	DL ROAKEEIH	LITOLF ADI	299
HlyD	KBAVLEQENK	Y EAANBELRV	YKSOLEIES	LSAKEEYQ	L TOLPKNI	300
MbxD	LES LROTNEQ	INQYTG TNR	AKQROKLLSI	SPVNGT TO	LTA TLGGVV	347
LktD	LEKL KOHIEN	EROLRLLELEK	NNORRQASMI	RAPVSGTVQQ	LKIHTIGGGV	349
ApXID	LEKL KQNV EA	EKQLSLLELEK	NEORQHASVI	RAPVSGTVQQ	LKTHTVGGVV	349
HlyD	LEKL ROTTLS	IELLTLELEK	NE ROQASVI	RAPVSGRVQQ	LKVHTEGGVV	350
MbxD	QAATK MVTA	FNDNQVEVEV	LVLNKDIGFV	KAGONV IIK	ESFPYTRYGY	397
LktD	TTAETLM IV	PEDDVLEATA	LVPNKDIGFV	AAGQEV IIKV	ETFPYTRYGY	399
ApXID	TTAETLMVIA	PEDDVLEVTA	L QNKDIGFI	EVGQDA I K V	ETFPYTRYGY	399
HlyD	TTAETLMVIV	PEDDTLEVTA	L VQNKDIGFI	NV GQNAI I K V	EAFPYTRYGY	400
MbxD	LTGRIKSI SH	DAIEHQHLGL	VNTA VSDT	STLN IDGVT	INLT PGMNVT	446
LktD	LTGRIKHISP	DAIEQPNVGL	VFNATIAIDR	KNLTSPDG K	IDLSSGMT T	449
ApXID	LMGKVRKNITL	AI EHPQLGL	VFNSTI SIDR	KTLSGKDGKE	IELGSGMSVT	449
HlyD	LVGKVRKNINL	DATEDQKLGL	VFNVI V S E	NDLST GNRH	IFLSSGMAVT	449
MbxD	ARIKTGKR RV	MDYLSPLT	KVDESFRER	475	SEQ ID NO: 37	
LktD	ARIKTGERSV	MSYLLSPLEE	SVTESLRER	478	SEQ ID NO: 38	
ApXID	ARIKTGERSV	ISYLLSPLEE	SVSES LRER	478	SEQ ID NO: 39	
HlyD	ARIKTGMRSV	ISYLLSPLEE	SVTESLHER	478	SEQ ID NO: 40	

F16.14

Cumulative Number of Calves With Severe Ulcers



Number of calves with ulcers with clinical scores >+2

F1615

Number of calves affected each week

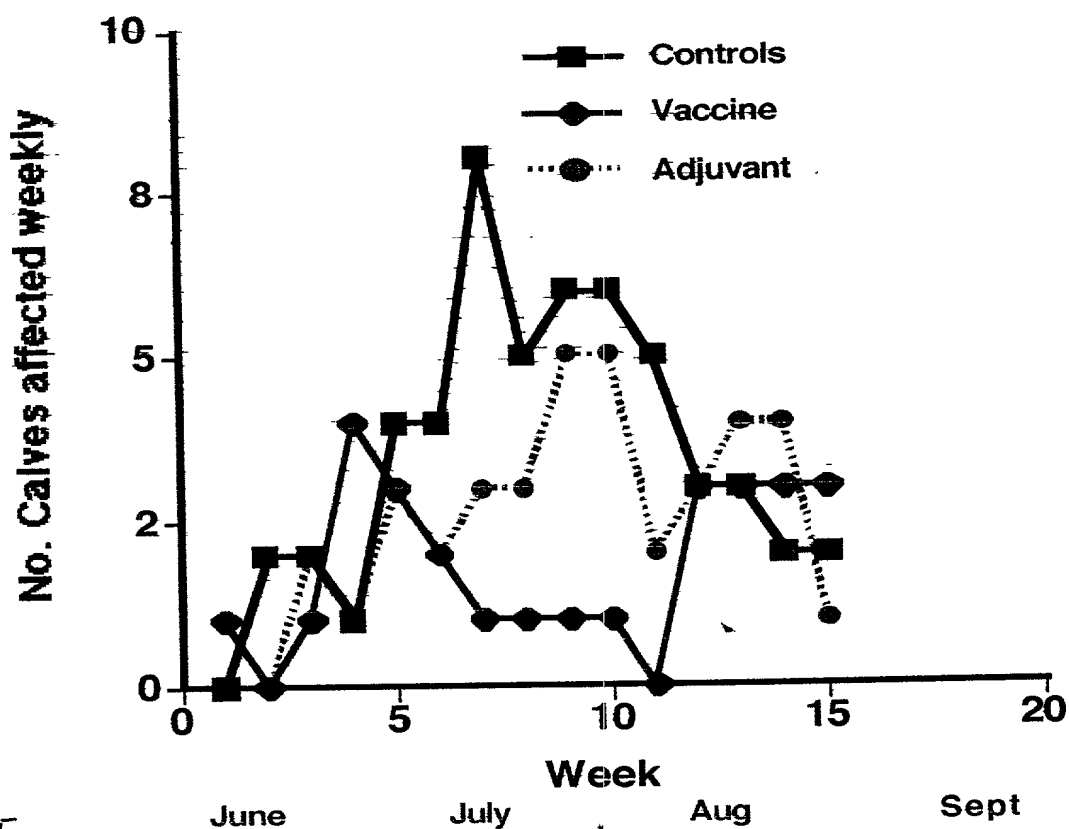
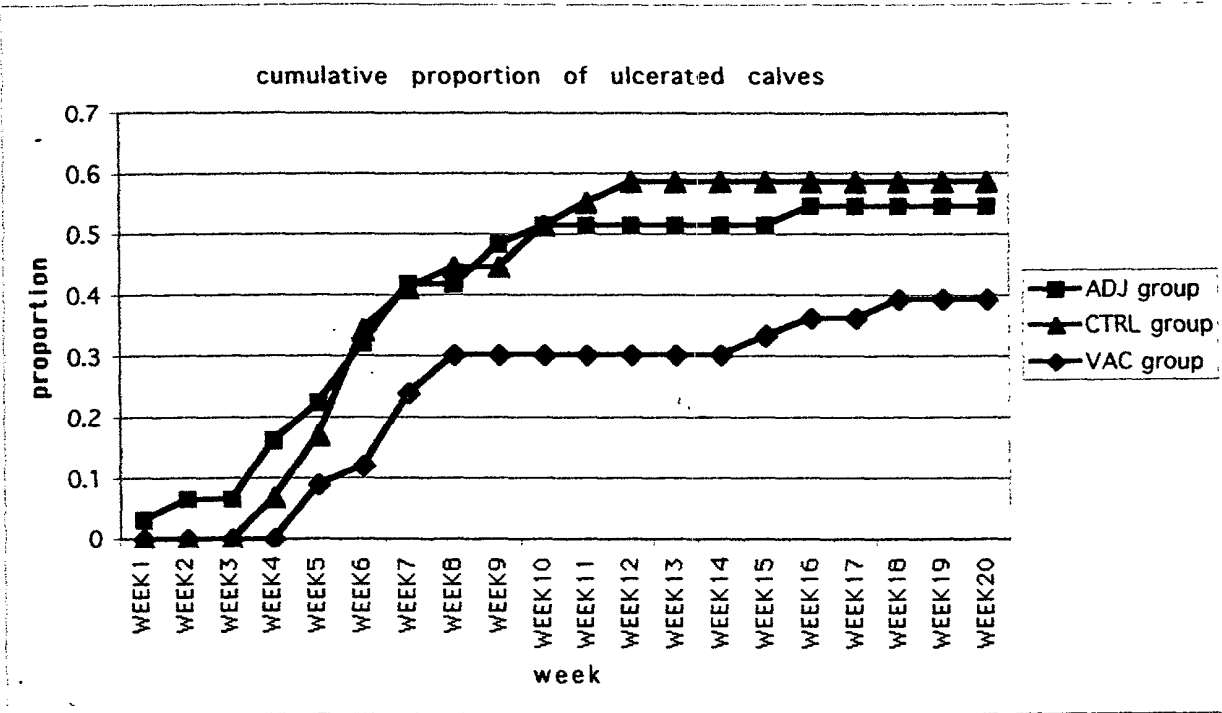


Figure 15
Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').